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Preliminary Results of the Determination of the Crystal Structure of ALE-1 C-terminus

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Beamline(s): X25

Results: Native PAGE was used to screen heavy atoms that may have high affinity for ALE-1, the protein under investigation. Meanwhile, we were able to harvest some high quality single crystals on another protein, Se-Met lysostaphin, which has ~80% sequence identity to ALE-1. Several high resolution (up to ~2Å) data sets were obtained at the NSLS X25 beamline, including MAD data (~2.5Å) for Se-Met lysostaphin, and ALE-1 heavy atom (platinum compounds, iradium compounds, osmium compounds, and et al.) data sets with scaled anomalous signals for possible MIR/MIRAD/SIR/SIRAD phasing. Preliminary results indicate that, although these two proteins have extremely high sequence identity and the protein crystals can be grown under fairly similar conditions, they crystallize in different space groups, P212121 for ALE-1 and I432 for lysostaphin. Original data have been processed using various program packages to search for the initial phase. Current and future work will involve electron density interpretation and more data collection if necessary.

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